RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: __10 084,507 A__
Source: __OIPE__
Date Processed by STIC: __7 12 02__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
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TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
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   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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   2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10|084,507A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Does Not Comply OIPE
Corrected Diskette Needed

See also p. 12

RAW SEQUENCE LISTING   DATE: 07/02/2002
PATENT APPLICATION: US/10/084,507A   TIME: 10:05:44

delete

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                  Input Set : A:\100879_1.asc
                  Output Set: N:\CRF3\07022002\J084507A.raw

W-->  1 (15)
      4 <110> APPLICANT: MUNROE, Donald G.
      5        KAMBOJ, Rajender
      6        PETERS, Diana
      7        KOOSHESH, Fatemeh
      8        VYAS, Tejal B.
      9        GUPTA, Ashwani K.
     11 <120> TITLE OF INVENTION: IDENTIFICATION OF LYSOLIPID RECEPTORS INVOLVED IN
     12        INFLAMMATORY RESPONSE
     14 <130> FILE REFERENCE: 8074-8021
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/084,507A
C--> 17 <141> CURRENT FILING DATE: 2002-06-14
     19 <150> PRIOR APPLICATION NUMBER: 60/109,885
     20 <151> PRIOR FILING DATE: 1998-11-25
     22 <150> PRIOR APPLICATION NUMBER: 60/080,610
     23 <151> PRIOR FILING DATE: 1998-04-03
     25 <150> PRIOR APPLICATION NUMBER: 60/070,185
     26 <151> PRIOR FILING DATE: 1997-12-30
     28 <160> NUMBER OF SEQ ID NOS: 25
     30 <170> SOFTWARE: PatentIn Ver. 2.1
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See error summary sheet item 1

global error: nucleic numbering must be placed at the end of the line, on the right margin

ERRORED SEQUENCES

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     32 <210> SEQ ID NO: 1
     33 <211> LENGTH: 35
     34 <212> TYPE: DNA
     35 <213> ORGANISM: Rattus sp.
     37 <400> SEQUENCE: 1
E--> 38 gagaaggttc aggaacacta caattacacc aagga                    35
     39 (35)
     42 <210> SEQ ID NO: 2
     43 <211> LENGTH: 25
     44 <212> TYPE: DNA
     45 <213> ORGANISM: Artificial Sequence
     47 <220> FEATURE:
     48 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
     49        primer
     51 <400> SEQUENCE: 2
E--> 52 attataccaa ggagacgctg gaaac                               25
     53 (25)
     56 <210> SEQ ID NO: 3
     57 <211> LENGTH: 25
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RAW SEQUENCE LISTING   DATE: 07/02/2002
PATENT APPLICATION: US/10/084,507A   TIME: 10:05:44

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 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 63        primer
 65 <400> SEQUENCE: 3
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 67 25
 70 <210> SEQ ID NO: 4
 71 <211> LENGTH: 22
 72 <212> TYPE: DNA
 73 <213> ORGANISM: Artificial Sequence
 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 77        primer
 79 <400> SEQUENCE: 4
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 81 22
 84 <210> SEQ ID NO: 5
 85 <211> LENGTH: 26
 86 <212> TYPE: DNA
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 89 <220> FEATURE:
 90 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
 91        primer
 93 <400> SEQUENCE: 5
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 95 26
 98 <210> SEQ ID NO: 6
 99 <211> LENGTH: 26
100 <212> TYPE: DNA
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
105        primer
107 <400> SEQUENCE: 6
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E--> 108 gagccccacc atgggcagct tgtact
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109 26
112 <210> SEQ ID NO: 7
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115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
119        primer
121 <400> SEQUENCE: 7
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E--> 122 gcattcacaa gaaattactc tgaggc
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123 26
126 <210> SEQ ID NO: 8
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RAW SEQUENCE LISTING   DATE: 07/02/2002
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Output Set: N:\CRF3\07022002\J084507A.raw

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131 <220> FEATURE:
132 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
133       primer
135 <400> SEQUENCE: 8
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137 34
140 <210> SEQ ID NO: 9
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143 <213> ORGANISM: Artificial Sequence
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146 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
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163 <400> SEQUENCE: 10
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E--> 164 tatatatcta gaggaaatgt gacgaggaga gg
```
165 32
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170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
175       primer
177 <400> SEQUENCE: 11
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E--> 178 tttaaaggta ccgccaccat gggcagcttg tac
```
179 33
182 <210> SEQ ID NO: 12
183 <211> LENGTH: 33
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic
189       primer
191 <400> SEQUENCE: 12
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E--> 192 tatatatcta gagaccaccg tgttgccctc cag
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193 33
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Input Set : A:\100879_1.asc
Output Set: N:\CRF3\07022002\J084507A.raw

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      197 <211> LENGTH: 445
      198 <212> TYPE: DNA
      199 <213> ORGANISM: Homo sapiens
      201 <400> SEQUENCE: 13
E--> 202 aaagccccat ggccccagca ggcctctgag ccccaccatg ggcagcttgt actcggagta
     203 60
E--> 204 cctgaacccc aacaaggtcc aggaacacta taattatacc aaggagacgc tggaaacgca
     205 120
E--> 206 ggagacgacc tcccgccagg tggcctcggc attcatcgtc atcctctgtt gcgccattgt
     207 180
E--> 208 ggtggaaaac cttctggtgc tcattgcggt ggcccgaaac agcaagttcc actcggcaat
     209 240
E--> 210 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc
     211 300
E--> 212 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg
     213 360
E--> 214 ggacggtctg ccttcatcac gctctcggcc tctgtcttca gcctcctggc catcgccatt
     215 420
E--> 216 gagcgccacg tggccattgc aaagg
     217 445
      220 <210> SEQ ID NO: 14
      221 <211> LENGTH: 364
      222 <212> TYPE: DNA
      223 <213> ORGANISM: Homo sapiens
      225 <400> SEQUENCE: 14
E--> 226 aaagccccat ggccccagca ggcctctgag ccccaccatg ggcagcttgt actcggagta
     227 60
E--> 228 cctgaacccc aacaaggtcc aggaacacta taattatacc aaggagacgc tggaaacgca
     229 120
E--> 230 ggagacgacc tcccgccagg tggcctcggc cttcatcgtc atcctctgtt gcgccattgt
     231 180
E--> 232 ggtggaaaac cttctggtgc tcattgcggt ggcccgaaac agcaagttcc actcggcaat
     233 240
E--> 234 gtacctgttt ctgggcaacc tggccgcctc cgatctactg gcaggcgtgg ccttcgtagc
     235 300
E--> 236 caataccttg ctctctggct ctgtcacgct gaggctgacg cctgtgcagt ggtttgcccg
     237 360
E--> 238 ggac
     239 364
      242 <210> SEQ ID NO: 15
      243 <211> LENGTH: 369
      244 <212> TYPE: DNA
      245 <213> ORGANISM: Homo sapiens
      247 <400> SEQUENCE: 15
E--> 248 agttctgaaa gccccatggc cccagcaggc ctctgagccc caccatgggc agcttgtact
     249 60
E--> 250 cggagtacct gaaccccaac aaggtccagg aacactataa ttataccaag gagacgctgg
     251 120
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          Input Set : A:\100879_1.asc
          Output Set: N:\CRF3\07022002\J084507A.raw

E--> 252 aaacgcagga gacgacctcc cgccaggtgg gctcggcctt catcgtcatc ctctgttgcg
     253 180
E--> 254 ccattgtggt ggaaaacctt ctggtgctca ttgcggtggc ccgaaacagc aagttccact
     255 240
E--> 256 cggcaatgta cctgtttctg ggcaacctgg ccgcctccga tctactggca ggcgtggctt
     257 300
E--> 258 cgtagccaat accttgctct ctggctctgt cacgctgagg ctgacgcctg tgcagtggtt
     259 360
E--> 260 tgcccggga
     261 369
     264 <210> SEQ ID NO: 16
     265 <211> LENGTH: 1170
     266 <212> TYPE: DNA
     267 <213> ORGANISM: Homo sapiens
     269 <220> FEATURE:
     270 <221> NAME/KEY: CDS
     271 <222> LOCATION: (38)..(1096)
     273 <400> SEQUENCE: 16
E--> 274 aaagccccat ggccccagca ggcctctgag ccccacc atg ggc agc ttg tac tcg
     275 55
     276   Met Gly Ser Leu Tyr Ser
     277   1   5
E--> 279 gag tac ctg aac ccc aac aag gtc cag gaa cac tat aat tat acc aag
     280 103
     281 Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu His Tyr Asn Tyr Thr Lys
     282   10   15   20
E--> 284 gag acg ctg gaa acg cag gag acg acc tcc cgc cag gtg gcc tcg gcc
     285 151
     286 Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser Arg Gln Val Ala Ser Ala
     287   25   30   35
E--> 289 ttc atc gtc atc ctc tgt tgc gcc att gtg gtg gaa aac ctt ctg gtg
     290 199
     291 Phe Ile Val Ile Leu Cys Cys Ala Ile Val Val Glu Asn Leu Leu Val
     292   40   45   50
E--> 294 ctc att gcg gtg gcc cga aac agc aag ttc cac tcg gca atg tac ctg
     295 247
     296 Leu Ile Ala Val Ala Arg Asn Ser Lys Phe His Ser Ala Met Tyr Leu
     297 55   60   65   70
E--> 299 ttt ctg ggc aac ctg gcc gcc tcc gat cta ctg gca ggc gtg gcc ttc
     300 295
     301 Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu Leu Ala Gly Val Ala Phe
     302   75   80   85
E--> 304 gta gcc aat acc ttg ctc tct ggc tct gtc acg ctg agg ctg acg cct
     305 343
     306 Val Ala Asn Thr Leu Leu Ser Gly Ser Val Thr Leu Arg Leu Thr Pro
     307   90   95   100
E--> 309 gtg cag tgg ttt gcc cgg gag ggc tct gcc ttc atc acg ctc tcg gcc
     310 391
     311 Val Gln Trp Phe Ala Arg Glu Gly Ser Ala Phe Ile Thr Leu Ser Ala

```
        312           105                   110                   115
E--> 314 tct gtc ttc agc ctc ctg gcc atc gcc att gag cgc cac gtg gcc att
     315 439
     316 Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg His Val Ala Ile
     317    120                   125                   130
E--> 319 gcc aag gtc aag ctg tat ggc agc gac aag agc tgc cgc atg ctt ctg
     320 487
     321 Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys Ser Cys Arg Met Leu Leu
     322 135                   140                   145                   150
E--> 324 ctc atc ggg gcc tcg tgg ctc atc tcg ctg gtc ctc ggt ggc ctg ccc
     325 535
     326 Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu Val Leu Gly Gly Leu Pro
     327                   155                   160                   165
E--> 329 atc ctt ggc tgg aac tgc ctg ggc cac ctc gag gcc tgc tcc act gtc
     330 583
     331 Ile Leu Gly Trp Asn Cys Leu Gly His Leu Glu Ala Cys Ser Thr Val
     332                   170                   175                   180
E--> 334 ctg cct ctc tac gcc aag cat tat gtg ctg tgc gtg gtg acc atc ttc
     335 631
     336 Leu Pro Leu Tyr Ala Lys His Tyr Val Leu Cys Val Val Thr Ile Phe
     337                   185                   190                   195
E--> 339 tcc atc atc ctg ttg gcc atc gtg gcc ctg tac gtg cgc atc tac tgc
     340 679
     341 Ser Ile Ile Leu Leu Ala Ile Val Ala Leu Tyr Val Arg Ile Tyr Cys
     342    200                   205                   210
E--> 344 gtg gtc cgc tca agc cac gct gac atg gcc gcc ccg cag acg cta gcc
     345 727
     346 Val Val Arg Ser Ser His Ala Asp Met Ala Ala Pro Gln Thr Leu Ala
     347 215                   220                   225                   230
E--> 349 ctg ctc aag acg gtc acc atc gtg cta ggc gtc ttt atc gtc tgc tgg
     350 775
     351 Leu Leu Lys Thr Val Thr Ile Val Leu Gly Val Phe Ile Val Cys Trp
     352                   235                   240                   245
E--> 354 ctg ccc gcc ttc agc atc ctc ctt ctg gac tat gcc tgt ccc gtc cac
     355 823
     356 Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp Tyr Ala Cys Pro Val His
     357                   250                   255                   260
E--> 359 tcc tgc ccg atc ctc tac aaa gcc cac tac ytt ttc gcc gtc tcc acc
     360 871
W--> 361 Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr Xaa Phe Ala Val Ser Thr
     362                   265                   270                   275
E--> 364 ctg aat tcc ctg ctc aac ccc gtc atc tac acg tgg cgc agc cgg gac
     365 919
     366 Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr Thr Trp Arg Ser Arg Asp
     367    280                   285                   290
E--> 369 ctg cgg cgg gag gtg ctt cgg ccg ctg cag tgc tgg cgg ccg ggg gtg
     370 967
     371 Leu Arg Arg Glu Val Leu Arg Pro Leu Gln Cys Trp Arg Pro Gly Val
     372 295                   300                   305                   310
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Input Set : A:\100879_1.asc
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E--> 374 ggg gtg caa gga cgg agg cgg ggc ggg acc ccg ggc cac cac ctc ctg
     375 1015
     376 Gly Val Gln Gly Arg Arg Arg Gly Gly Thr Pro Gly His His Leu Leu
     377   315   320   325
E--> 379 cca ctc cgc agc tcc agc tcc ctg gag agg ggc atg cac atg ccc acg
     380 1063
     381 Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg Gly Met His Met Pro Thr
     382   330   335   340
E--> 384 tca ccc acg ttt ctg gag ggc aac acg gtg gtc tgagggtggg ggtggaccaa
     385 1116
     386 Ser Pro Thr Phe Leu Glu Gly Asn Thr Val Val
     387   345   350
E--> 389 caaccaggcc agggcatagg ggttcatgga aaggccactg ggtgacccca aata
     390 1170
     393 <210> SEQ ID NO: 17
     394 <211> LENGTH: 353
     395 <212> TYPE: PRT
     396 <213> ORGANISM: Homo sapiens
     398 <400> SEQUENCE: 17
     399 Met Gly Ser Leu Tyr Ser Glu Tyr Leu Asn Pro Asn Lys Val Gln Glu
     400   1   5   10   15
     402 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
     403   20   25   30
     405 Arg Gln Val Ala Ser Ala Phe Ile Val Ile Leu Cys Cys Ala Ile Val
     406   35   40   45
     408 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
     409   50   55   60
     411 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
     412   65   70   75   80
     414 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
     415   85   90   95
     417 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
     418   100   105   110
     420 Phe Ile Thr Leu Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile
     421   115   120   125
     423 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Asp Lys
     424   130   135   140
     426 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
     427 145   150   155   160
     429 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
     430   165   170   175
     432 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
     433   180   185   190
     435 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
     436   195   200   205
     438 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
     439   210   215   220
     441 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
     442 225   230   235   240

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      444 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
      445             245             250             255
      447 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
      448             260             265             270
E--> 450 Xaa Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
      451             275             280             285
      453 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
      454     290             295             300
      456 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Gly Gly Thr
      457 305             310             315             320
      459 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
      460             325             330             335
      462 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
      463             340             345             350
      465 Val
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      471 <211> LENGTH: 1170
      472 <212> TYPE: DNA
      473 <213> ORGANISM: Homo sapiens
      475 <400> SEQUENCE: 18
E--> 476 tttcggggta ccggggtcgt ccggagactc ggggtggtac ccgtcgaaca tgagcctcat
      477 60
E--> 478 ggacttgggg ttgttccagg tccttgtgat attaatatgg ttcctctgcg acctttgcgt
      479 120
E--> 480 cctctgctgg agggcggtcc accggagccg gaagtagcag taggagacaa cgcggtaaca
      481 180
E--> 482 ccaccttttg gaagaccacg agtaacgcca ccgggctttg tcgttcaagg tgagccgtta
      483 240
E--> 484 catggacaaa gacccgttgg accggcggag gctagatgac cgtccgcacc ggaagcatcg
      485 300
E--> 486 gttatggaac gagagaccga gacagtgcga ctccgactgc ggacacgtca ccaaacgggc
      487 360
E--> 488 cctcccgaga cggaagtagt gcgagagccg gagacagaag tcggaggacc ggtagcggta
      489 420
E--> 490 actcgcggtg caccggtaac ggttccagtt cgacataccg tcgctgttct cgacggcgta
      491 480
E--> 492 cgaagacgag tagccccgga gcaccgagta gagcgaccag gagccaccgg acgggtagga
      493 540
E--> 494 accgaccttg acggacccgg tggagctccg gacgaggtga caggacggag agatgcggtt
      495 600
E--> 496 cgtaatacac gacacgcacc actggtagaa gaggtagtag gacaaccggt agcaccggga
      497 660
E--> 498 catgcacgcg tagatgacgc accaggcgag ttcggtgcga ctgtaccggc ggggcgtctg
      499 720
E--> 500 cgatcgggac gagttctgcc agtggtagca cgatccgcag aaatagcaga cgaccgacgg
      501 780
E--> 502 gcggaagtcg taggaggaag acctgatacg gacagggcag gtgaggacgg gctaggagat
      503 840
E--> 504 gtttcgggtg atgraaaagc ggcagaggtg ggacttaagg gacgagttgg ggcagtagat
```

RAW SEQUENCE LISTING   DATE: 07/02/2002
PATENT APPLICATION: US/10/084,507A   TIME: 10:05:44

Input Set : A:\100879_1.asc
Output Set: N:\CRF3\07022002\J084507A.raw

```
      505 900
E--> 506 gtgcaccgcg tcggccctgg acgccgccct ccacgaagcc ggcgacgtna cgaccgccgg
      507 960
E--> 508 cccccacccc cacgttcctg cctccgcccc gccctggggc ccggtggtgg aggacggtga
      509 1020
E--> 510 ggcgtcgagg tcgagggacc tctccccgta cgtgtacggg tgcagtgggt gaaaagacct
      511 1080
E--> 512 cccgttgtgc caccagactc ccacccccac ctggttgttg gtccggtccc gtatccccaa
      513 1140
E--> 514 gtacctttcc ggtgacccac tggggtttat
      515 1170
      518 <210> SEQ ID NO: 19
      519 <211> LENGTH: 1062
      520 <212> TYPE: DNA
      521 <213> ORGANISM: Homo sapiens
      523 <400> SEQUENCE: 19
E--> 524 atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat
      525 60
E--> 526 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcatc
      527 120
E--> 528 gtcatcctct gttgcgccat tgtggtggaa aaccttctgg tgctcattgc ggtggcccga
      529 180
E--> 530 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta
      531 240
E--> 532 ctggcaggcg tggccttcgt agccaatacc ttgctctctg gctctgtcac gctgaggctg
      533 300
E--> 534 acgcctgtgc agtggtttgc ccgggagggc tctgccttca tcacgctctc ggcctctgtc
      535 360
E--> 536 ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat
      537 420
E--> 538 ggcagcgaca agagctgccg catgcttctg ctcatcgggg cctcgtggct catctcgctg
      539 480
E--> 540 gtcctcggtg gcctgcccat ccttggctgg aactgcctgg ccacctcga ggcctgctcc
      541 540
E--> 542 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtgaccat cttctccatc
      543 600
E--> 544 atcctgttgg ccgtcgtggc cctgtacgtg cgcatctact gcgtggtccg ctcaagccac
      545 660
E--> 546 gctgacatgg ccgccccgca gacgctagcc ctgctcaaga cggtcaccat cgtgctaggc
      547 720
E--> 548 gtctttatcg tctgctggct gcccgccttc agcatcctcc ttctggacta tgcctgtccc
      549 780
E--> 550 gtccactcct gcccgatcct ctacaaagcc cactaccttt tcgccgtctc caccctgaat
      551 840
E--> 552 tccctgctca accccgtcat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt
      553 900
E--> 554 cggccgctgc agtgctggcg gccggggtg ggggtgcaag gacggaggcg gggcgggacc
      555 960
E--> 556 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg
```

```
        557 1020
E--> 558 cccacgtcac ccacgtttct ggagggcaac acggtggtct ga
        559 1062
        562 <210> SEQ ID NO: 20
        563 <211> LENGTH: 1062
        564 <212> TYPE: DNA
        565 <213> ORGANISM: Homo sapiens
        567 <400> SEQUENCE: 20
E--> 568 tacccgtcga acatgagcct catggacttg gggttgttcc aggtccttgt gatattaata
        569 60
E--> 570 tggttcctct gcgacctttg cgtcctctgc tggagggcgg tccaccggag ccggaagtag
        571 120
E--> 572 cagtaggaga caacgcggta acaccacctt ttggaagacc acgagtaacg ccaccgggct
        573 180
E--> 574 ttgtcgttca aggtgagccg ttacatggac aaagacccgt tggaccggcg gaggctagat
        575 240
E--> 576 gaccgtccgc accggaagca tcggttatgg aacgagagac cgagacagtg cgactccgac
        577 300
E--> 578 tgcggacacg tcaccaaacg ggccctcccg agacggaagt agtgcgagag ccggagacag
        579 360
E--> 580 aagtcggagg accggtagcg gtaactcgcg gtgcaccggt aacggttcca gttcgacata
        581 420
E--> 582 ccgtcgctgt tctcgacggc gtacgaagac gagtagcccc ggagcaccga gtagagcgac
        583 480
E--> 584 caggagccac cggacgggta ggaaccgacc ttgacggacc cggtggagct ccggacgagg
        585 540
E--> 586 tgacaggacg gagagatgcg gttcgtaata cacgacacgc accactggta gaagaggtag
        587 600
E--> 588 taggacaacc ggcagcaccg ggacatgcac gcgtagatga cgcaccaggc gagttcggtg
        589 660
E--> 590 cgactgtacc ggcggggcgt ctgcgatcgg gacgagttct gccagtggta gcacgatccg
        591 720
E--> 592 cagaaatagc agacgaccga cgggcggaag tcgtaggagg aagacctgat acggacaggg
        593 780
E--> 594 caggtgagga cgggctagga gatgtttcgg gtgatggaaa agcggcagag gtgggactta
        595 840
E--> 596 agggacgagt tggggcagta gatgtgcacc gcgtcggccc tggacgccgc cctccacgaa
        597 900
E--> 598 gccggcgacg tcacgaccgc cggcccccac ccccacgttc ctgcctccgc cccgccctgg
        599 960
E--> 600 ggcccggtgg tggaggacgg tgaggcgtcg aggtcgaggg acctctcccc gtacgtgtac
        601 1020
E--> 602 gggtgcagtg ggtgcaaaga cctcccgttg tgccaccaga ct
        603 1062
        831 <210> SEQ ID NO: 24
        832 <211> LENGTH: 1056
        833 <212> TYPE: DNA
        834 <213> ORGANISM: Homo sapiens
        836 <400> SEQUENCE: 24
```

RAW SEQUENCE LISTING   DATE: 07/02/2002
PATENT APPLICATION: US/10/084,507A   TIME: 10:05:44

Input Set : A:\100879_1.asc
Output Set: N:\CRF3\07022002\J084507A.raw

```
E--> 837 atggtcatca tgggccagtg ctactacaac gagaccatcg gcttcttcta taacaacagt
     838 60
E--> 839 ggcaaagagc tcagctccca ctggcggccc aaggatgtgg tcgtggtggc actggggctg
     840 120
E--> 841 accgtcagcg tgctggtgct gctgaccaat ctgctggtca tagcagccat cgcctccaac
     842 180
E--> 843 cgccgcttcc accagcccat ctactacctg ctcggcaatc tggccgcggc tgacctcttc
     844 240
E--> 845 gcgggcgtgg cctacctctt cctcatgttc cacactggtc cccgcacagc ccgactttca
     846 300
E--> 847 cttgagggct ggttcctgcg gcagggcttg ctggacacaa gcctcactgc gtcggtggcc
     848 360
E--> 849 acactgctgg ccatcgccgt ggagcggcac cgcagtgtga tggccgtgca gctgcacagc
     850 420
E--> 851 cgcctgcccc gtggccgcgt ggtcatgctc attgtgggcg tgtgggtggc tgccctgggc
     852 480
E--> 853 ctggggctgc tgcctgccca ctcctggcac tgcctctgtg ccctggaccg ctgctcacgc
     854 540
E--> 855 atggcacccc tgctcagccg ctcctatttg gccgtctggg ctctgtcgag cctgcttgtc
     856 600
E--> 857 ttcctgctca tggtggctgt gtacacccgc attttcttct acgtgcggcg gcgagtgcag
     858 660
E--> 859 cgcatggcag agcatgtcag ctgccacccc cgctaccgag agaccacgct cagcctggtc
     860 720
E--> 861 aagactgttg tcatcatcct gggggcgttc gtggtctgct ggacaccagg ccaggtggta
     862 780
E--> 863 ctgctcctgg atggtttagg ctgtgagtcc tgcaatgtcc tggctgtaga aaagtacttc
     864 840
E--> 865 ctactgctgg ccgaggccaa ctcactggtc aatgctgctg tgtactcttg ccgagatgct
     866 900
E--> 867 gagatgcgcc gcaccttccg ccgccttctc tgctgcgcgt gcctccgcca gtccacccgc
     868 960
E--> 869 gagtctgtcc actatacatc ctctgcccag ggaggtgcca gcactcgcat catgcttccc
     870 1020
E--> 871 gagaacggcc acccactgat ggactccacc ctttag
     872 1056
```

VARIABLE LOCATION SUMMARY   DATE: 07/02/2002
PATENT APPLICATION: US/10/084,507A   TIME: 10:05:45

Input Set : A:\100879_1.asc
Output Set: N:\CRF3\07022002\J084507A.raw

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:16; Xaa Pos. 273
Seq#:17; Xaa Pos. 273
Seq#:18; N Pos. 949

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/084,507A

DATE: 07/02/2002
TIME: 10:05:45

Input Set : A:\100879_1.asc
Output Set: N:\CRF3\07022002\J084507A.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:38 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:35 SEQ:1
L:52 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:2
L:66 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:3
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:4
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:5
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:6
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:7
L:136 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:34 SEQ:8
L:150 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:9
L:164 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:10
L:178 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:11
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:12
L:202 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:13
M:254 Repeated in SeqNo=13
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
M:254 Repeated in SeqNo=14
L:248 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15
M:254 Repeated in SeqNo=15
L:274 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:55 SEQ:16
M:254 Repeated in SeqNo=16
L:361 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:871
L:450 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:476 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:18
M:254 Repeated in SeqNo=18
M:340 Repeated in SeqNo=18
L:524 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:568 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:20
M:254 Repeated in SeqNo=20
L:837 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:24
M:254 Repeated in SeqNo=24
L:881 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:25
M:254 Repeated in SeqNo=25